<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/700, 313A_
Source: _1FW16_
Date Processed by STIC: _3/21/06_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 03/21/2006
PATENT APPLICATION: US/10/700,313A   TIME: 08:49:52

Input Set : **A:\seq listing.app**
Output Set: **N:\CRF4\03212006\J700313A.raw**

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  3 <110> APPLICANT: Combadiere et al.
  5 <120> TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS AND
THERAPEUTIC
  6         AGENTS FOR HIV INFECTION
  8 <130> FILE REFERENCE: 66645-01
 10 <140> CURRENT APPLICATION NUMBER: US 10/700,313A
 11 <141> CURRENT FILING DATE: 2003-10-31
 13 <150> PRIOR APPLICATION NUMBER: US 60/018,508
 14 <151> PRIOR FILING DATE: 1996-05-28
 16 <150> PRIOR APPLICATION NUMBER: 08/864,458
 17 <151> PRIOR FILING DATE: 1997-05-28
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: PatentIn version 3.3
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 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
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 38 tat gac atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg       101
 39 Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val
 40 10                  15                  20                  25
 42 aag caa atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc       149
 43 Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
 44                 30                  35                  40
 46 atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac       197
 47 Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn
 48                 45                  50                  55
 50 tgc aaa agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc       245
 51 Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala
 52         60                  65                  70
 54 atc tct gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tac       293
 55 Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr
 56     75                  80                  85
 58 ttg gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca       341
 59 Leu Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr
 60 90                  95                  100                 105
 62 ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc       389
 63 Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu
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68             125            130            135
70 aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg    485
71 Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
72         140            145            150
74 gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct    533
75 Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser
76     155            160            165
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79 Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser
80 170            175            180            185
82 cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg    629
83 Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu
84             190            195            200
86 ggg ctg gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc    677
87 Gly Leu Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile
88         205            210            215
90 cta aaa act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct    725
91 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
92     220            225            230
94 gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct    773
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98 ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc    821
99 Pro Tyr Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly
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119 Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
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147         35                  40                  45
150 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
151     50                  55                  60
154 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
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159             85                  90                  95
162 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
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166 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
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174 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
175 145                 150                 155                 160
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179             165                 170                 175
182 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
183             180                 185                 190
186 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
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190 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
191     210                 215                 220
194 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
195 225                 230                 235                 240
198 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
199             245                 250                 255
202 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
203             260                 265                 270
206 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
207         275                 280                 285
210 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
211     290                 295                 300
214 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
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218 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
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229 <213> ORGANISM: Homo sapiens
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233 <221> NAME/KEY: CDS
234 <222> LOCATION: (27)..(1082)
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242 Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val
243 10                  15              20                  25
245 aag caa atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc       149
246 Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
247                 30              35                  40
249 atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac       197
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255             60              65                  70
257 atc tct gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tat       293
258 Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr
259     75              80                  85
261 gct gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca       341
262 Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr
263 90              95              100                 105
265 ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc       389
266 Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu
267             110             115                 120
269 ctg aca atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta       437
270 Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu
271             125             130                 135
273 aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg       485
274 Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
275             140             145                 150
277 gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct       533
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279     155             160                 165
281 caa aaa gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt       581
282 Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser
283 170             175                 180                 185
285 cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg       629
286 Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu
287             190             195                 200
289 ggg ctg gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc       677
290 Gly Leu Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile
291             205             210                 215
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293 cta aaa act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct    725
294 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
295         220                 225                 230
297 gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct    773
298 Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala
299     235                 240                 245
301 ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc    821
302 Pro Tyr Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly
303 250                 255                 260                 265
305 ctg aat aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg    869
306 Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val
307                 270                 275                 280
309 aca gag act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat    917
310 Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr
311             285                 290                 295
313 gcc ttt gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa    965
314 Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln
315         300                 305                 310
317 aag cac att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa    1013
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321 gag gct ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag    1061
322 Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
323 330                 335                 340                 345
325 cag gaa ata tct gtg ggc ttg tgacacggac tcaagtgggc tggtgaccca      1112
326 Gln Glu Ile Ser Val Gly Leu
327                 350
329 gtcagagttg tgcacatggc ttagttttca tacacagcct gggctggggg tggggtggga   1172
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350         35                  40                  45
353 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
354     50                  55                  60
357 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
358 65                  70                  75                  80
361 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
362             85                  90                  95
365 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
366             100                 105                 110
369 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/21/2006
PATENT APPLICATION: US/10/700,313A   TIME: 08:49:53

Input Set : **A:\seq listing.app**
Output Set: **N:\CRF4\03212006\J700313A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 1

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10

VERIFICATION SUMMARY   DATE: 03/21/2006
PATENT APPLICATION: US/10/700,313A   TIME: 08:49:53

Input Set : **A:\seq listing.app**
Output Set: **N:\CRF4\03212006\J700313A.raw**

L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0